

IAP5 Rec'd PCT/PTO 31 JUL 2006

## 【Sequence Listing】

&lt;110&gt; Lifenza Co., Ltd.

5 <120> PROTEIN WITH ACTIVITY OF HYDROLYZING DEXTRAN, STARCH, MUTAN,  
INULIN AND LEVANN, GENE ENCODING THE SAME, CELL EXPRESSING THE  
SAME, AND PRODUCTION METHOD THEREOF

&lt;150&gt; KR2004-0006185

&lt;151&gt; - 2004-01-30

10

&lt;160&gt; 4

&lt;170&gt; KopatentIn 1.71

15

&lt;210&gt; 1

&lt;211&gt; 608

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

20

&lt;220&gt;

&lt;223&gt; S. cerevisiae/pYES2-LS01

&lt;400&gt; 1

25

Met Thr Leu Ile Tyr Val Pro Ser Ile Phe Thr Met Val Pro Ser Ile

1

5

10

15

Thr Arg Ile Val Leu Val Asn Ile Leu Leu Ala Thr Leu Val Leu Gly

20

25

30

30

Ala Ala Val Leu Pro Arg Asp Asn Arg Thr Val Cys Gly Ser Gln Leu

35

40

45

Cys Thr Trp Trp His Asp Ser Gly Glu Ile Asn Thr Gly Thr Pro Val

35

50

55

60

Gln Ala Gly Asn Val Arg Gln Ser Arg Lys Tyr Ser Val His Val Ser

65                      70                      75                      80  
 Leu Ala Asp Arg Asn Gln Phe Tyr Asp Ser Phe Val Tyr Glu Ser Ile  
                                  85                      90                      95  
 5  
 Pro Arg Asn Gly Asn Gly Arg Ile Tyr Ser Pro Thr Asp Pro Pro Asn  
                                  100                      105                      110  
 Ser Asn Thr Leu Asn Ser Ser Ile Asp Asp Gly Ile Ser Ile Glu Pro  
 10                      115                      120                      125  
 Ser Leu Gly Ile Asn Met Ala Trp Ser Gln Phe Glu Tyr Arg Arg Asp  
                                  130                      135                      140  
 15 Val Asp Ile Lys Ile Thr Thr Ile Asp Gly Ser Ile Leu Asp Gly Pro  
                                  145                      150                      155                      160  
 Leu Asp Ile Val Ile Arg Pro Thr Ser Val Lys Tyr Ser Val Lys Arg  
                                  165                      170                      175  
 20 Cys Val Gly Gly Ile Ile Ile Arg Val Pro Tyr Asp Pro Asn Gly Arg  
                                  180                      185                      190  
 Lys Phe Ser Val Glu Leu Lys Ser Asp Leu Tyr Ser Tyr Leu Ser Asp  
 25                      195                      200                      205  
 Gly Ser Gln Tyr Val Thr Ser Gly Gly Ser Val Val Gly Val Glu Pro  
                                  210                      215                      220  
 30 Lys Asn Ala Leu Val Ile Phe Ala Ser Pro Phe Leu Pro Arg Asp Met  
                                  225                      230                      235                      240  
 Val Pro His Met Thr Pro His Asp Thr Gln Thr Met Lys Pro Gly Pro  
                                  245                      250                      255  
 35 Ile Asn Asn Gly Asp Trp Gly Ser Lys Pro Ile Leu Tyr Phe Pro Pro  
                                  260                      265                      270

Gly Val Tyr Trp Met Asn Glu Asp Thr Ser Gly Asn Pro Gly Lys Leu  
 275 280 285

5 Gly Ser Asn His Met Arg Leu Asp Pro Asn Thr Tyr Trp Val His Leu  
 290 295 300

Ala Pro Gly Ala Tyr Val Lys Gly Ala Ile Glu Tyr Phe Thr Lys Gln  
 305 — 310 315 320

10 Asn Phe Tyr Ala Thr Gly His Gly Val Leu Ser Gly Glu Asn Tyr Val  
 325 330 335

Tyr`Gln Ala Asn Ala Ala Asp Asn Tyr Tyr Ala Val Lys Ser Asp Gly  
 15 340 345 350

Thr Ser Leu Arg Met Trp Trp His Asn Asn Leu Gly Gly Gly Gln Thr  
 355 360 365

20 Trp Phe Cys Met Gly Pro Thr Ile Asn Ala Pro Pro Phe Asn Thr Met  
 370 375 380

Asp Phe Asn Gly Asn Ser Asn Ile Ser Ser Arg Ile Ser Asp Tyr Lys  
 385 390 395 400

25 Gln Val Gly Ala Tyr Phe Phe Gln Thr Asp Gly Pro Glu Ile Tyr Glu  
 405 410 415

Asp Ser Val Val His Asp Val Phe Trp His Val Asn Asp Asp Ala Ile  
 30 420 425 430

Lys Thr Tyr Tyr Ser Gly Ala Ser Ile Ser Arg Ala Thr Ile Trp Lys  
 435 440 445

35 Cys His Asn Asp Pro Ile Ile Gln Met Gly Trp Thr Ser Arg Asn Leu  
 450 455 460

Thr Gly Ile Ser Ile Asp Asn Leu His Val Ile His Thr Arg Tyr Phe  
 465 470 475 480  
 Lys Ser Glu Thr Val Val Pro Ser Ala Ile Ile Gly Ala Ser Pro Phe  
 5 485 490 495  
 Tyr Ala Ser Gly Met Thr Val Asp Pro Ser Glu Ser Ile Ser Met Thr  
 500 505 510  
 10 Ile Ser Asn Val Val Cys Glu Gly Leu Cys Pro Ser Leu Phe Arg Ile  
 515 520 525  
 Thr Pro Leu Gln Ser Tyr Asn Asn Leu Val Val Lys Asn Val Ala Phe  
 530 535 540  
 15 Pro Asp Gly Leu Gln Thr Asn Pro Ile Gly Ile Gly Glu Ser Ile Ile  
 545 550 555 560  
 Pro Ala Ala Ser Gly Cys Thr Met Asp Leu Glu Ile Thr Asn Trp Thr  
 20 565 570 575  
 Val Lys Gly Gln Lys Val Thr Met Gln Asn Phe Gln Ser Gly Ser Leu  
 580 585 590  
 25 Gly Gln Phe Asp Ile Asp Gly Ser Tyr Trp Gly Gln Trp Ser Ile Asn  
 595 600 605

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<210> 2  
 <211> 2052  
 <212> DNA  
 <213> Artificial Sequence

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<220>  
 <221> S. cerevisiae/pYLS01

<400> 2  
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 cgacgttggc tttgggagct gcagtccttc cagagacaa cagaactgtt tgcgggagtc 180  
 —  
 10 aactctgcac atggtggcac gactccggcg agataaacac cggctactcct gtacaggcag 240  
 gaaacgttcg acaatcccg aagtactctg tccatgtgag cctggcagac cgtaaccaat 300  
 tctacgactc tttcgtatat gaatcgatac ctaggaacgg caatggcaga atttatctc 360  
 15 ccaccgaccc acctaacagc aatacattga atagtagcat tgacgacggc atatcaatcg 420  
 aaccaictct cggcataac atggcttggc ccagttcga atatagcga gatgtcgaca 480  
 20 ttaagattac tacaatcgat ggctcaatat tggatggccc ttggacatt gttattcggc 540  
 cgacttctgt taagtactca gtcaaaagat gtgtgggtgg tatcattatt agagtcacct 600  
 atgatcccaa tggtcgaaaa ttctctgttg agttaagag tgacctttac agttacctct 660  
 25 ccgacggttc gcaatatgtg acctctggag ggagcgttgt tgggtggag ccaaaaaatg 720  
 ccctggatgat ctttgccagc cctttcttgc cacgggatat ggttcctcat atgacaccac 780  
 30 acgacacca gacaatgaag ccgggcccaa tcaataatgg ggactggggt tcaaagccta 840  
 tactctactt cccgcctggc gtatactgga tgaacgagga tacctctggt aaccccgga 900  
 agctcggctc aaatcataig cggctggatc ccaataccta ctgggtccat ctgccccag 960  
 35 gagcctatgt gaaaggagcc attgagtatt tcacgaagca aaatttctat gcaacgggtc 1020

	atggcgttct ctcaggtgag aactatgttt atcaggccaa tgcagctgat aactactatg	1080
	ccgtcaagag tgatggcaca agcttgagaa tgtggtggca caacaacctt ggaggcggtc	1140
5	aaacatggtt ttgcatgggg cccaccatta atgcaccgcc gttaataacg atggacttca	1200
	acggaaactc taatatttcc agccggatta gtgactataa gcaggttggc gcttattttt	1260
	tccaaacaga cggaccggag atctacgagg acagtgttgt ccatgacgtc ttctggcatg	1320
10	ttaatgatga tgccatcaag acatattatt cggagcttc aatttcacga gcaaccatct	1380
	ggaagtgtca caatgaccog atcatacaga tgggctggac gtcacgaaat ctcaccggaa	1440
15	tcagcattga taacctgcac gtcattccaca cgagatattt caaatctgaa acagtggttc	1500
	cttcagcaat cattggagcg tctccattct acgcaagtgg aatgactgtt gatcccagcg	1560
	agtccatcag catgaccatc tctaacgtgg tgtgtgaggg tctatgccc tcactgttcc	1620
20	gtatcactcc gcttcagagc tacaacaacc ttgttgtcaa gaacgtggcc ttccccgatg	1680
	gactgcagac aaatccaatc ggaataggag agagcattat accagcagct tccggctgta	1740
25	caatggactt ggaaatcaca aactggaccg tcaaaggaca aaaagtcacc atgcaaaact	1800
	ttcagtcogg gtcacttggc cagttcgata tcgatggttc atactgggtt caatggtcca	1860
	taactaaag ctattcccat tcacctgagt attttcgtgg gtccaatgag ttcttgttac	1920
30	tgatggggcc cttgctagtg gtaaaagtag agggacttgt cctcgccggg cgccaaggaa	1980
	gttcatgtct tctagttgaa tagtatttgt ttcttctctc tcgttaaaaa aaaaaaaaaa	2040
35	aaaaaaaaaa aa	2052

<210> 3  
<211> 18  
<212> DNA  
<213> Artificial Sequence

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<220>  
<223> L. starkeyi DX-F primer(sense)

10 <400> 3  
gtcccttgag ctcccaac

18

15 <210> 4  
<211> 23  
<212> DNA  
<213> Artificial Sequence

20 <220>  
<223> L. starkeyi DX-R primer(antisense)

<400> 4  
tcaactagaa ttcatagaact tcc  
25

23